

## Figure 1

bcl Consensus PCR Primers

Ile

EcoRI AspTrpGlyArgValValAla

5- AGATCTGAATTCAACTTGGGGGIC(A)GIA(G)TXGTXGC -3' bclx 1-32

AspTrpGlyGlyGlnGluAsnAspGlnIleTrp

AGGGTIGGIGGXACXAGA(G)ACA(T)(C)TAGGT

5'- AGATCT'AAGCTTGTCCCAICCCICCTGXTCC(T)TGA(G)ATCCA -3' bclX 2-39

Figure 2

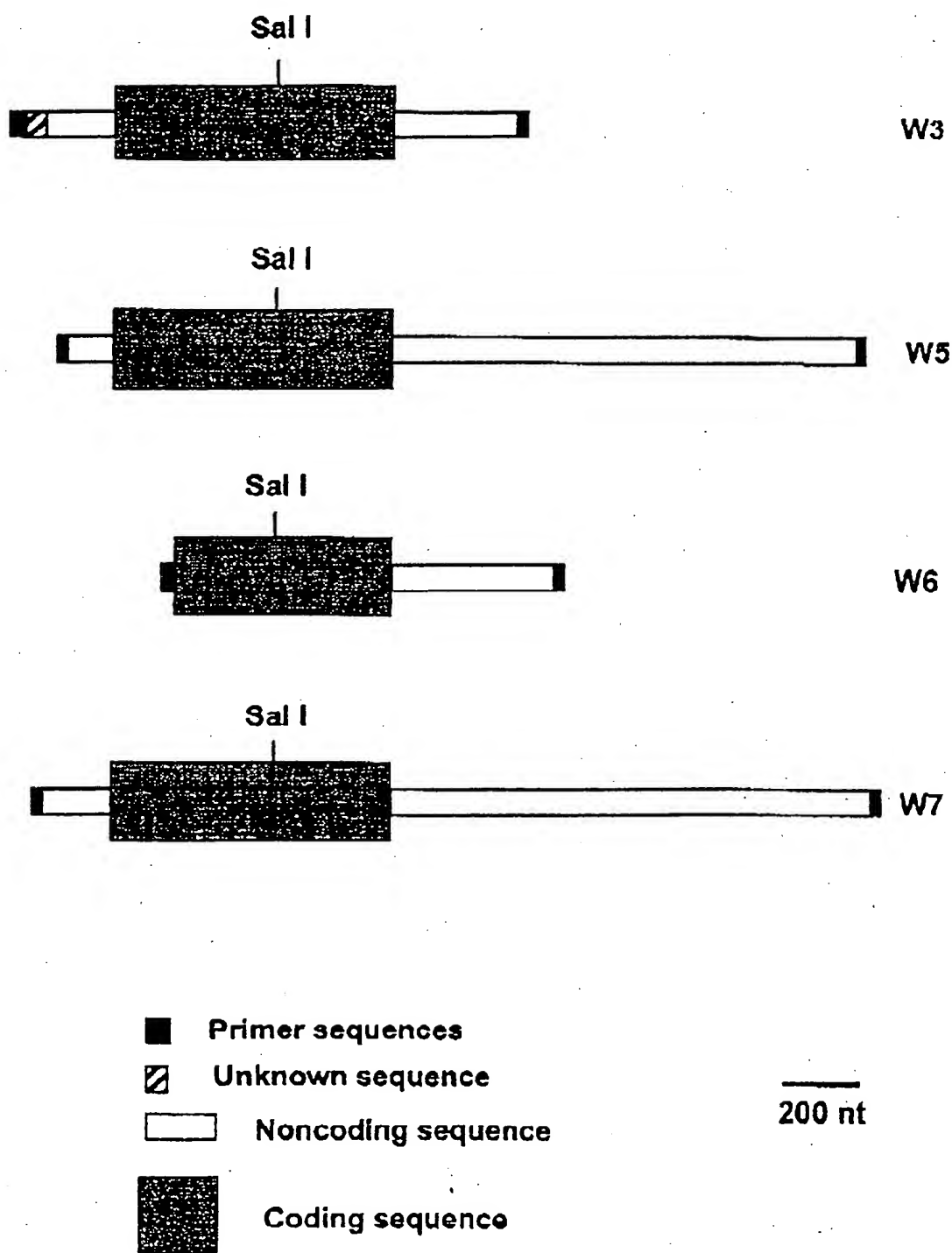
**Cdi-1 cDNA clones**

Figure 3

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      10      20      30      40
      *      *      *      *
GAG GAT CTA CAG GGG ACA AGT AAA GGC TAC ATC CAG ATG CCG GGA ATG
CTC CTA GAT GTC CCC TGT TCA TTT CCG ATG TAG GTC TAC GGC CCT TAC

>Aha2
50      60      70      80      90
*      *      *      *      *
CAC TGA CGC CCA TTC CTG GAA ACT GGG CTC CCA CTC AGC CCC TGG GAG
GTG ACT GCG GGT AAG GAC CTT TGA CCC GAG GGT GAG TCG GGG ACC CTC

100      110      120      130      140
*      *      *      *      *
CAG CAG CCG CCA GCC CCT CGG ACC TCC ATC TCC ACC CTG CTG AGC CAC
GTC GTC GGC GGT CGG GGA GCC TGG AGG TAG AGG TGG GAC GAC TCG GTG

>SmaI      >BamHI
150      160      170      180      190
*      *      *      *      *
CCG GGT TGG GCC AGG ATC CCG GCA GGC TGA TCC CGT CCT CCA CTG AGA
GGC CCA ACC CGG TCC TAG GGC CCT CCG ACT AGG GCA GGA GGT GAC TCT

200      210      220      230      240
*      *      *      *      *
CCT GAA AA ATG GCT TCG GGG CAA GGC CCA GGT CCT CCC AGG CAG GAG TGC
GGA CTT TT TAC CGA AGC CCC GTT CCG GGT CCA GGA GGG TCC GTC CTC ACG
      M A S G Q G P G P P R Q E C>

250      260      270      280      290
*      *      *      *      *
GGA GAG CCT GCC CTG CCC TCT GCT TCT GAG GAG CAG GTA GCC CAG GAC
CCT CTC CGA CCG GAC GGG AGA CGA AGA CTC CTC GTC CAT CCG GTC CTG
G E P A L P S A S E E Q V A Q D>

300      310      320      330
*      *      *      *
ACA GAG GAG GTT TTC CGC AGC TAC GTT TTT TAC CGC CAT CAG CAG GAA
TGT CTC CTC CAA AAG GCG TCG ATG CAA AAA ATG GCG GTA GTC GTC CTT
T E E V F R S Y V F Y R H Q Q E>

340      350      360      370      380
*      *      *      *      *
CAG GAG GCT GAA GGG GTG GCT GCC CCT GCC GAC CCA GAG ATG GTC ACC
GTC CTC CGA CTT CCC CAC CGA CCG GGA CCG CTG GGT CTC TAC CAG TGG
Q E A E G V A A P A D P E M V T>

>NcoI
390      400      410      420      430
*      *      *      *      *
TTA CCT CTG CAA CCT AGC AGC ACC ATG GGG CAG GTG GGA CCG CAG CTC
AAT GGA GAC GTT GGA TCG TCG TGG TAC CCC GTC CAC CCT GCC GTC GAG
L P L Q P S S T M G Q V G R Q L>

440      450      460      470      480
*      *      *      *      *
GCC ATC ATC GGG GAC GAC ATC AAC CGA CGC TAT GAC TCA GAG TTC CAG
CGG TAG TAG CCC CTG CTG TAG TTG SCT GCG ATA CTG AGT CTC AAG GTC

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Figure 3 cont.

A I I G D D I N R R Y D S E F Q>

>Pst1

490                      500                      510                      520                      530

\*                      \*                      \*                      \*                      \*

ACC ATG TTG CAG CAC CTG CAG CCC ACG GCA GAG AAT GCC TAT GAG TAC  
TGG TAC AAC GTC GTG GAC CTC GGG TGC CGT CTC TTA CCG ATA CTC ATG  
T M L Q H L Q P T A E N A Y E Y>

540                      550                      560                      570

\*                      \*                      \*                      \*

TTC ACC AAG ATT GCC ACC AGC CTG TTT GAG AGT GGC ATC AAT TGG GGC  
AAG TGG TTC TAA CCG TGG TCG GAC AAA CTC TCA CCG TAG TTA ACC CCG  
F T K I A T S L F E S G I N W G>

580                      590                      600                      610                      620

\*                      \*                      \*                      \*                      \*

CGT GTG GTG GGT CTT CTG GGC TTC GGC TAC CGT CTG GCC CTA CAC GTC  
GCA CAC CAC CGA GAA GAC CCG AAG CCG ATG GCA GAC CCG GAT GTG CAG  
R V V A L L G F G Y R L A L H V>

630                      640                      650                      660                      670

\*                      \*                      \*                      \*                      \*

TAC CAG CAT GGC CTG ACT GGC TTC CTA GGC CAG GTG ACC CGC TTC GTG  
ATG GTC GTA CCG GAC TGA CCG AAG GAT CCG GTC CAC TGG GCG AAG CAC  
Y Q H G L T G F L G Q V T R F V>

>Seq11

680                      690                      700                      710                      720

\*                      \*                      \*                      \*                      \*

GTC GAC TTC ATG CTG CAT CAC TGC ATT GCC CGG TGG ATT GCA CAG AGG  
CAG CTG AAG TAC GAC GTA GTG ACG TAA CCG GCC ACC TAA CGT GTC TCC  
V D F M L H H C I A R W I A Q R>

730                      740                      750                      760                      770

\*                      \*                      \*                      \*                      \*

GGT GGC TGG GTG GCA GCC CTG AAC TTG GGC AAT GGT CCC ATC CTG AAC  
CCA CCG ACC CAC CGT CCG GAC TTG AAC CCG TTA CCA GGG TAG GAC TTG  
G G W V A A L N L G N G P I L N>

780                      790                      800                      810

\*                      \*                      \*                      \*

GTG CTG GTG GTT CTG GGT GTG GTT CTG TTG GGC CAG TTT GTG GTA CGA  
CAC GAC CAC CAA GAC CCA CAC CAA GAC AAC CCG GTC AAA CAC CAT GCT  
V L V V L G V V L L G Q F V V R>

820                      830                      840                      850                      860

\*                      \*                      \*                      \*                      \*

AGA TTC TTC AAA TCA TGA C TCC CAA GGC TGC CCT TTG GGT CCC GGT TCA  
TCT AAG AAG TTT AGT ACT G AGG GTT CCC ACG GGA AAC CCA GGG CCA AGT  
R F F K S \*>

>Af12

870                      880                      890                      900                      910

\*                      \*                      \*                      \*                      \*

GAC CCC TGC CTG GAC TTA AGC GAA GTC TTT GGC CAG TTT GTG GTA CGA  
CTG GGG ACG GAC CTG AAT TCG CTT CAG AAA CCG AAG AGA CAA GGG AAC

&gt;Hind3

Figure 3 cont.

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      920      930      940      950      960
      *      *      *      *      *
CAG GGT CCC CCC TCA AGA GTA CAG AAG CTT TAG CAA GTG TGC ACT CCA
GTC CCA GGG GGG AGT TCT CAT GTC TTC GAA ATC GTT CAC ACG TGA GGT

                                     >PstI
      970      980      990      1000      1010
      *      *      *      *      *
GCT TCG GAG GCC CTG CGT GGG GGC CAG TCA GGC TGC AGA GGC ACC TCA
CGA AGC CTC CGG GAC GCA CCC CCG GTC AGT CCG ACG TCT CCG TGG AGT

                                     >ApaI
      1020      1030      1040      1050
      *      *      *      *
ACA TTG CAT GGT GCT AGT GCC CTC TCT CTG GGC CCA GGG CTG TGG CCG
TGT AAC GTA CCA CGA TCA CGG GAG AGA GAC CCG GGT CCC GAC ACC GGC

1060      1070      1080      1090      1100
      *      *      *      *      *
TCT CCT CCC TCA GCT CTC TGG GAC CTC CTT AGC CCT GTC TGC TAG GCG
AGA GGA GGG AGT CGA GAG ACC CTG GAG GAA TCG GGA CAG ACG ATC CGC

1110      1120      1130      1140      1150
      *      *      *      *      *
CTG GGG AGA CTG ATA ACT TGG GGA GGC AAG AGA CTG GGA GCC ACT TCT
GAC CCC TCT GAC TAT TGA ACC CCT CCG TTC TCT GAC CCT CCG TGA AGA

      1160      1170      1180      1190      1200
      *      *      *      *      *
CCC CAG AAA GTG TTT AAC GGT TTT AGC TTT TTA TAA TAC CCT TGT GAG
GGG GTC TTT CAC AAA TTG CCA AAA TCG AAA AAT ATT ATG GGA ACA CTC

                                     >Aha2
      1210      1220      1230      1240      1250
      *      *      *      *      *
AGC CCA TTC CCA CCA TTC TAC CTG AGG CCA GGA CGT CTG GGG TGT GGG
TCG GGT AAG GGT GGT AAG ATG GAC TCC GGT CCT GCA GAC CCC ACA CCC

      1260      1270      1280      1290
      *      *      *      *
GAT TGG TGG GTC TAT GTT CCC CAG GAT TCA GCT AAT CTG GAA GAT CAG
CTA ACC ACC CAG ATA CAA GGG GTC CTA AGT CGA TAA GAC CTT CTA GTC

1300      1310      1320      1330      1340
      *      *      *      *      *
CAC CCT AAG AGA TGG GAC TAG GAC CTG AGC CTG GTC CTG GCC GTC CCT
GPG GGA TTC TCT ACC CTG ATC CTG GAC TCG GAC CAG GAC CCG CAG GGA

1350      1360      1370      1380      1390
      *      *      *      *      *
AAG CAT GTG TCC CAG GAG CAG GAC CTA CTA GGA GAG GGG GGC CAA GGT
TTC GTA CAC AGG GTC CTC GTC CTG GAT GAT CCT CTC CCC CCG GTT CCA

      1400      1410      1420      1430      1440
      *      *      *      *      *
CCT GCT CAA CTC TAC CCC TGC TCC CAT TCC TCC CTC CCG CCA TAC TGC
GGA CGA GTT GAG ATG GGG ACG AGG GTA AAG AGG GAG GCC GGT ATG ACG

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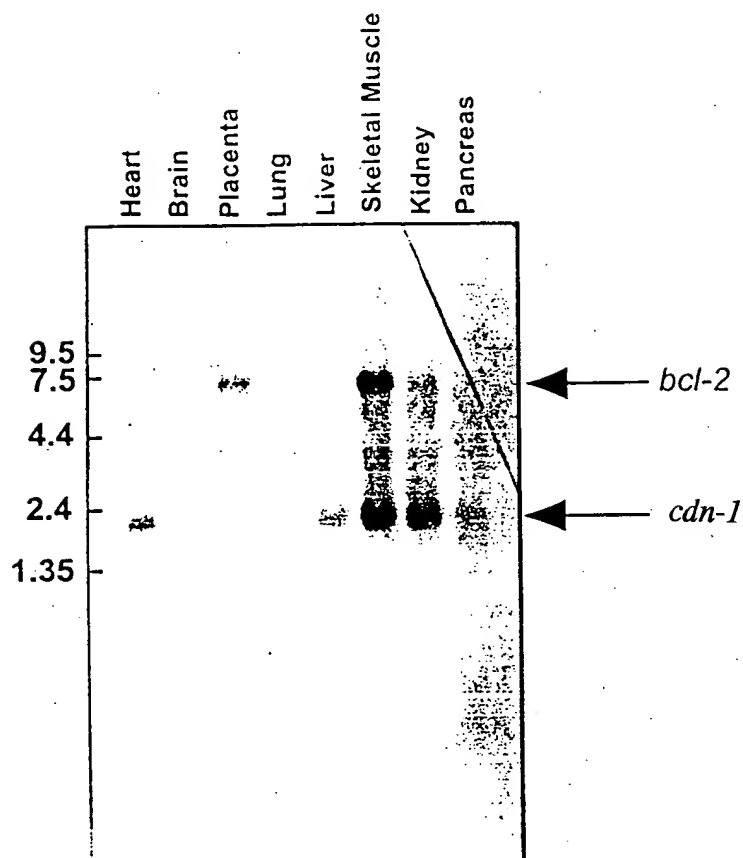
## Figure 3 cont.

1450 * CTT TGC AGT TGG ACT CTC AGG GAT TCT GGG CTT GGG GTG TGG GGT GGG GAA ACG TCA ACC TGA GAG TCC CTA AGA CCC GAA CCC CAC ACC CCA CCC	1460 * 1500 * GTG GAG TCG CAG ACC AGA GCT GTC TGA ACT CAC GTG TCA GAA GCC TCC CAC CTC AGC GTC TGG TCT CGA CAG ACT TGA GTG CAC AGT CTT CGG AGG	1470 * 1510 * 1520 * 1530 *	1480 * 1540 * 1550 * 1560 * 1570 * 1580 *	1490 * 1590 * 1600 * 1610 * 1620 * 1630 *
AAG CCT GCC TCC CAA GGT CCT CTC AGT TCT CTC CCT TCC TCT CTC CTT TTC GGA CGG AGG GGT CCA GGA GAG TCA AGA GAG GGA AGG AGA GAG GAA	ATA GAC ACT TGC TCC CAA CCC ATT CAC TAC AGG TGA AGG CTC TCA CCC TAT CTG TGA ACG AGG GTT GGG TAA GTG ATG TCC ACT TCC GAG AGT GGG	1640 * 1650 * 1660 * 1670 * 1680 *	1690 * 1700 * 1710 * 1720 * 1730 *	1740 * 1750 * 1760 * 1770 *
ATC CCT GGG GGC CTT GGG TGA GTG GCC TGC TAA GGC TCC TCC TTG CCC TAG GGA CCC CCG GAA CCC ACT CAC CGG ACG ATT CCG AGG AGG AAC GGG	AGA CTA CAG GGC TTA GGA CTT GGT TTG TTA TAT CAG GGA AAA GGA GTA TCT GAT GTC CCG AAT CCT GAA CCA AAC AAT ATA GTC CCT TTT CCT CAT	GGG AGT TCA TCT GGA GGG TTC TAA GTG GGA GAA GGA CTA TCA ACA CCA CCC TCA AGT AGA CCT CCC AAG ATT CAC CCT CTT CCT GAT AGT TGT GGT		
>BamH1				
1780 * CTA GGA ATC CCA GAG GTG GAT CCT CCC TCA TGG CTC TGG CAC AGT GTA GAT CCT TAG GGT CTC CAC CTA GGA GGG AGT ACC GAG ACC GTG TCA CAT	1790 * 1800 * 1810 * 1820 *	1830 * 1840 * 1850 * 1860 * 1870 *	1880 * 1890 * 1900 * 1910 * 1920 *	1930 * 1940 * 1950 * 1960 * 1970 *
ATC CAG GGG TGT AGA TGG GGG AAC TGT GAA TAC TTG AAC TCT GTT CCC TAG GTC CCC ACA TCT ACC CCC TTG ACA CTT ATG AAC TTG AGA CAA GGG	CCA CCC TCC ATG CTC CTC ACC TGT CTA GGT CTC CTC AGG GTG GGG GGT GGT GGG AGG TAC GAG GAG TGG ACA GAT CCA GAG GAG TCC CAC CCC CCA	GAC AGT GCC TTC TCT ATT GGC ACA GCC TAG GGT CTT GGG GGT CAG GGG CTG TCA CGG AAG AGA TAA CCG TGT CGG ATC CCA GAA CCC CCA GTC CCC	1980 * 1990 * 2000 * 2010 *	
GGA GAA GTT CTT GAT TCA GCC AAA TGC AGG GAG GGG AGG CAG ATG GAG CCT CTT CAA GAA CTA AGT CGG TTT ACG TCC CTC CCC TCC GTC TAC CTC				

## Figure 3 cont.

2020	2030	2040	2050	2060											
*	*	*	*	*											
CCC	ATA	GGC	CAC	CCC	CTA	TCC	TCT	GAG	TGT	TTG	GAA	ATA	AAC	TGT	GCA
GGG	TAT	CCG	GTG	GGG	GAT	AGG	AGA	CTC	ACA	AAC	CTT	TAT	TTG	ACA	CGT
2070	2080	2090													
*	*	*													
ATC	CCC	TCA	AAA	AAA	AAA	CGG	AGA	TCC							
TAG	GGG	AGT	TTT	TTT	TTT	GCC	TCT	AGG							

Figure 4

Multiple Tissue Northern  
*bcl-2* and *cdn-1* hybridization

Random primed, Klenow-labeled fragments of *bcl-2* and *cdn-1* clones were hybridized to a multiple human tissue Northern blot (Clontech 7760-1), at a final concentration of  $1 \times 10^6$  cpm/ml for each probe. Blot was washed at high stringency.



Figure 5

cdn-2 gene sequence

```

      10          20          30          40          50          60
      *          *          *          *          *          *
TTT TAA TAT AAA TTA ATG TGC TCT ATT TAT AGA GAC AAT ACA TGA AAT ATA CTT AAT AAA
AAA ATT ATA TTT AAT TAC ACG AGA TAA ATA TCT CTG TTA TGT ACT TTA TAT GAA TTA TTT

      70          80          90          100          110          120
      *          *          *          *          *          *
AAT TCA AAT GTT ATA GAA CTG AAA AAG ATG AAA AGT AAA AAC AAC CTA TTC CCC AGA GGT
TTA AGT TTA CAA TAT CTT GAC TTT TTC TAC TTT TCA TTT TTG TTG GAT AAG GGG TCT CCA

      130          140          150          160          170          180
      *          *          *          *          *          *
AGC CAC TGT CCA TAG TTT CTA TTT TAG ATT CTT TCC TTT ATA CAA GAT TAT TAT AGC TTC
TCG GTG ACA GGT ATC AAA GAT AAA ATC TAA GAA AGG AAA TAT GTT CTA ATA ATA TCG AAG

      190          200          210          220          230          240
      *          *          *          *          *          *
TAT TTT TTG GTG TAT GAA CTG TAG TCC TAG AGG ATT TTA TTA GTT ATG AGT TCT ATA ACT
ATA AAA AAC CAC ATA CTT GAC ATC AGG ATC TCC TAA AAT AAT CAA TAC TCA AGA TAT TGA

      250          260          270          280          290          300
      *          *          *          *          *          *
AAG ATC CAT CAT CTT AGT TGC TAA GAA CGT AGA TAC TGA GAA CAT CAT TTA AAA AAA CAT
TTC TAG GTA GTA GAA TCA ACG ATT CTT GCA TCT ATG ACT CTT GTA GTA AAT TTT TTT GTA

      310          320          330          340          350          360
      *          *          *          *          *          *
TTT TGG CTG GCA CCT CAT GAT CAC TGG AGT CTC GCG GGT CCC TCA GGC TGC ACA GGG ACA
AAA ACC GAC CGT GGA GTA CTA GTG ACC TCA GAG CGC CCA GGG AGT CCG ACG TGT CCC TGT

      370          380          390          400          410          420
      *          *          *          *          *          *
AGT AAA GGC TAC ATC CAG ATG CTG GGA ATG CAC TGA CGC CCA TTC CTG GAA ACT GGG CTC
TCA TTT CCG ATG TAG GTC TAC GAC CCT TAC GTG ACT GCG GGT AAG GAC CTT TGA CCC GAG

      430          440          450          460          470          480
      *          *          *          *          *          *
CCA CTC AGC CCC TGG GAG CAG CAG CCG CCA GCC CCT CGG GAC CTC CAT CTC CAC CCT GCT
GGT GAG TCG GGG ACC CTC GTC GTC GGC GGT CGG GGA GCC CTG GAG GTA GAG GTG GGA CGA

      490          500          510          520          530          540
      *          *          *          *          *          *
GAG CCA CCC GGG TTG GGC CAG GAT CCC GGC AGG CTG ATC CCG TCC TCC ACT GAG ACC TGA
CTC GGT GGG CCC AAC CCG GTC CTA GGG CCG TCC GAC TAG GGC AGG AGG TGA CTC TGG ACT

      550          560          570          580          590          600
      *          *          *          *          *          *
AAA ATG GCT TCG GGG CAA GGC CCA GGT CCT CCC AGG CAG GAG TGC GGA GAG CCT GCC CTG
TTT TAC CGA AGC CCC GTT CCG GGT CCA GGA GGG TCC GTC CTC ACG CCT CTC GGA CGG GAC
      M   A   S   G   Q   G   P   G   P   P   R   Q   E   C   G   E   P   A   L>

      610          620          630          640          650          660
      *          *          *          *          *          *
CCC TCT GCT TCT GAG GAG CAG GTA GCC CAG GAC ACA GAG GAG GTT TTC CGC AGC TAC GTT
GGG AGA CGA AGA CTC CTC GTC CAT CGG GTC CTG TGT CTC CTC CAA AAG GCG TCG ATG CAA
      P   S   A   S   E   E   Q   V   A   Q   D   T   E   E   V   F   R   S   Y   V>

      670          680          690          700          710          720
      *          *          *          *          *          *
TTT TAC CAC CAT CAG CAG GAA CAG GAG GCT GAA GGG GCG GCT GCC CCT GCC GAC CCA GAG
AAA ATG GTG GTA GTC GTC CTT GTC CTC CGA CTT CCC CGC CGA CGG GGA CGG CTG GGT CTC
      F   Y   H   H   Q   Q   E   Q   E   A   E   G   A   A   A   P   A   D   P   E>

```

Figure 5 cont.

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                                >NcoI
      730          740          750          760          770          780
      *          *          *          *          *          *
ATG GTC ACC TTA CCT CTG CAA CCT AGC AGC ACC ATG GGG CAG GTG GGA CGG CAG CTC GCC
TAC CAG TGG AAT GGA GAC GTT GGA TCG TCG TGG TAC CCC GTC CAC CCT GCC GTC GAG CGG
M V T L P L Q P S S T M G Q V G R Q L A>

      790          800          810          820          830          840
      *          *          *          *          *          *
ATC ATT GGG GAC GAC ATC AAC CGA CGC TAT GAC TCA GAG TTC CAG ACC ATG TTG CAG CAC
TAG TAA CCC CTG CTG TAG TTG GCT GCG ATA CTG AGT CTC AAG GTC TGG TAC AAC GTC GTG
I I G D D I N R R Y D S E F Q T M L Q H>

      >PstI
      850          860          870          880          890          900
      *          *          *          *          *          *
CTG CAG CCC ACG GCA GAG AAT GCC TAT GAG TAC TTC ACC AAG ATT GCC TCC AGC CTG TTT
GAC GTC GGG TGC CGT CTC TTA CGG ATA CTC ATG AAG TGG TTC TAA CGG AGG TCG GAC AAA
L Q P T A E N A Y E Y F T K I A S S L F>

      910          920          930          940          950          960
      *          *          *          *          *          *
GAG AGT GGC ATC AAT TGG GGC CGT GTG GTG GCT CTT CTG GGC TTC AGC TAC CGT CTG GCC
CTC TCA CCG TAG TTA ACC CCG GCA CAC CAC CGA GAA GAC CCG AAG TCG ATG GCA GAC CGG
E S G I N W G R V V A L L G F S Y R L A>

      970          980          990          1000          1010          1020
      *          *          *          *          *          *
CTA CAC ATC TAC CAG CGT GGC CTG ACT GGC TTC CTG GGC CAG GTG ACC CGC TTT GTG GTG
GAT GTG TAG ATG GTC GCA CCG GAC TGA CCG AAG GAC CCG GTC CAC TGG GCG AAA CAC CAC
L H I Y Q R G L T G F L G Q V T R F V V>

      1030          1040          1050          1060          1070          1080
      *          *          *          *          *          *
GAC TTC ATG CTG CAT CAC TGC ATT GCC CGG TGG ATT GCA CAG AGG GGT GGC TGG GTG GCA
CTG AAG TAC GAC GTA GTG ACG TAA CGG GCC ACC TAA CGT GTC TCC CCA CCG ACC CAC CGT
D F M L H H C I A R W I A Q R G G W V A>

      1090          1100          1110          1120          1130          1140
      *          *          *          *          *          *
GCC CTG AAC TTG GGC AAT GGT CCC ATC CTG AAC GTG CTG GTG GTT CTG GGT GTG GTT CTG
CGG GAC TTG AAC CCG TTA CCA GGG TAG GAC TTG CAC GAC CAC CAA GAC CCA CAC CAA GAC
A L N L G N G P I L N V L V V L G V V L>

      1150          1160          1170          1180          1190          1200
      *          *          *          *          *          *
TTG GGC CAG TTT GTG GTA CGA AGA TTC TTC AAA TCA TGA CTC CCA AGG GTG CCT TTG GGG
AAC CCG GTC AAA CAC CAT GCT TCT AAG AAG TTT AGT ACT GAG GGT TCC CAC GGA AAC CCC
L G Q F V V R R F F K S *>

      1210          1220          1230          1240          1250          1260
      *          *          *          *          *          *
TCC CAG TTC AGA CCC CTG CCT GGA CTT AAG CGA AGT CTT TGC CTT CTC TGC TCC TTG CAG
AGG GTC AAG TCT GGG GAC GGA CCT GAA TTC GCT TCA GAA ACG GAA GAG ACG AGG AAC GTC

                                >Hind3
      1270          1280
      *          *
GGT CCC CCC TCA AGA GTA CAG AAG CTT
CCA GGG GGG AGT TCT CAT GTC TTC GAA

```

Figure 6 Amino acid sequences of cdn-1, cdn-2, and bcl-2 family proteins

cdn1	masgggpppprqqecgepalpsaaseeqvaqdtteefrsyvfyrhqgeaeagvaapadpemt	
cdn2	masgggpppprqqecgepalpsaaseeqvaqdtteefrsyvfyrhqgeaeagvaapadpemt	
bcl2	mahagrtgyDNREIVMKYIHYKLSQGYEWdagvgaapqpfssqpghtphtaaardpvarspiqtpaapga	
bax	mdgsgeqprgggptseeqimktgalllqgfiqdragrmggaep	
bcl-x	msqSNRELVDVFLSYKLSQKGSWSqsfadveenrteaegtesemetpsaingnpswhladespavngatghsssl	
mcl-1	...(+123 aa)eldgyepeplgkrpavlpillelvgesGnntstdgslpstppaeeedelyrqaleiisrylreगतakdtk	
A1	maeselmhihsaehylgyvlq	
bhbf	maystreillalcirdsrvhngntlhpvlleaar	
LMW5-HL	megeeliyhniineilvgv	
ced9	mtrctadnsltnpayrrrtmatgemkeflgikgteptdfginsdaqdlpsprqastrmsigesidgkindweeprldIEGFVVVDYFTHRIRQNGMEWfgapg	
cdn1	lplqpsstmgQVGRQLAIIGDDINRRYDSEFQTMLOHLOPTAENAYEYFTKIATSLFESGI-NWGRVVALLGFGYRLALHVVYQHGLTGFLGQVTRFVVDFMLHH	
cdn2	lplqpsstmgQVGRQLAIIGDDINRRYDSEFQTMLOHLOPTAENAYEYFTKIATSLFESGI-NWGRVVALLGFGYRLALHVVYQHGLTGFLGQVTRFVVDFMLHH	
bcl2	agpalspvpvVHLTLRQAGDDFRRYRRDFAEMSRQLHLtpftargrfatvVEELFRDGV-NWGRIVAFTEFGGVMCVESVNRMSPLVDNIALWMTEY-LNR	
bax	elaldpvpqdaastkklsecikrigdeldsnmelgrmiaavtdsprevFFRVAADMFSDGNFNWGRVVALFYFASKLVLKALCTKVPDELIRTIMGTDLDF-LRE	
bcl-x	darevipma-AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFQVVMELFRDGV-NWGRIVAFTEFGGVMCVESVNRMSPLVDNIALWMTEY-LNR	
mcl-1	pmgrsgatsrkaLETTLRRVGDGVQRNHETVTFQGLRKLDIKNEDDVKSLSRVMIHVFSDDGVTNWGRIVTLISFGAFVAKHLKTINQESCIPLAESITD-VLVR	
A1	vpafesapsqacrvlgrvafsvqkeveknkysliddfhvesidtarliFNQVMEKEFEDGIINWGRIVTIFAFGGVLLKKLPQEQIALdvcaykqvsfvaefi	
bhbf	etplrlspedtvvlryhvlleelernsetftetwnrfithtehvdldfnsvfleifhd-LINWGRICGFIVFSARMAKYCKDANN-HLESTVITTAYNF-SEG	
LMW5-HL	ikyyymndihelspyqqiklityydeclnkqvtitfsltnaqeiklQFTGVVTELFKrgdpslgralamawcmhacrtlccnqstpyyvvdlsvrgmleam-	
ced9	lpcgvqpehemrvmgtifekkhaenfetfceglLavprisfslyqdvrvrtvgnagtqgcpMSYGRLLIGLISFGGFVAAKmesvelqgqvrvnlfvytslfiKT	
cdn1	CIAR--WIA-QR-GGWVAALNLGngpilnvlvlgvllgqvvrffks	SEQUENCE IDENTITY:
cdn2	CIAR--WIA-QR-GGWVAALNLGngpilnvlvlgvllgqvvrffks	cdn1/cdn2 = 97%
bcl2	HLHT--WI--QDNGGWDFAVELYgpsmrpldfswlskltslslalvgacitlgaylghk	
bax	RLLG--WI--QDQGGWDGLLSYfgtptqvtifvagvltasltiwwkmg	
bcl-x	HLEP--WI--QENGWDTFVELYgnnaaaesrkqgerfnrwlftgntvagvllgslfsrk	
mcl-1	TKRD--WLVKQ--RGWDGFVEFFhvedleggirvnllafagvagvagalylir	
A1	MNNTGEWI-RQ-NGWDEdgiikkfepksgwltflqmtgqiweamlfllk	
bhbf	-LDG--WIHQ--GGWStliednipgsrfrswtflagltlslvicsylfisargrh	
LMW5-HL	KHNLPPWMISH--GGQEEFLAFslhsqiyvifnikyflskfnhfrlscvqlirkcnli	
ced9	-RIRNNWKE-H-NRSWDDFMTLgkmkedyeraaeakvgrrkqnrrwsmigagvtagagivgvvvcgrmmfalk	

60  
 GAAPTCTGGT AATTAGTTAA AATACCTGA ACAACTTGT TCACTTCTCT GAGTCTCACT TTCTCACTCA AAAATGCTCA  
 120  
 ATAAATTGTA AACTTCTGGT AATAATCTAC GACTCTACAA GAGGCAATAG GGTACTGTGT ACAGAGAGCA GGTCTTGGA  
 180  
 ACACACAGA CTGGGTTTAG ATTCTCTCAC TCAACCACT GTGTGACTTG CCAAGCTTC TCACTTCTC TAAAGGCCCA  
 240  
 TCTGTGTATC TGTACAGGAA TGAATGAAG AGTATGTACA CCAAGCTAT CCAAGTCCA GGTTAATTA TTGCTTGGG  
 300  
 TTTTAACTA AATTGTTCAA GCTCATGACA TTCTAGGAGA AAAGGCTAG TGTCTCTTC TTAAGGTGAT TGTGTGATG  
 360  
 TGTCTTCCAG GAATCTATG GCTTCTCAA CCAATCTCA CCGTGGCTT GACCAATGG CTACCACTCT TCACTGATTC  
 420  
 TGTCTGATG ACACAACCTG CACTCAGCAT CTGCGCTGC AGCTAGATG GATTTCTAG TGGGCAATG CTGGGGGATA  
 480  
 CCACATGGCC ACCATGTCA CAGATTTCT GTTACAGTCC ACCCGGACC ATTCTTCTC AATCATAAI CCTTAAGCAG  
 540  
 GAGAGCTAGG TCCAGCACC ATGACATAA CACCAACCT TCGTACAAI CTCAGCTACT ATCTTGAATC TGAACCAAT  
 600  
 GTCTAGTGGC AGCGCGGCCC TTCTTTTCA AGAGATGCT GGGATCAGT CTTTTCACA AAGATGCTCT CCGCAGCTC  
 660  
 CTTTCTTCC AGGTCTGAC ACTGAAAGT AAGACAGCAT TTCTTACGC ATATTTCAAA AATTTGCTT ATACCTTCAT  
 720  
 CTCAGGACAA CAGTGGCTC CTTAAGAGCC TTATCTTGT GTACTTGTA TTTTCTTTC CCGTACCTT CCAAGGCTA  
 780  
 GTCTACTTC TCGCTGCTA CTTGAGCAA AGTCACTC AATATTTT AACTACCTT TTAGTGGC ACGGCAATT  
 840  
 ATTTTACCT TCGCAGAGC CTTAATTTGT CACTCTGAC ATAGCAGTAC CTTCAGCAC CTGAGGACA ATACATTT  
 900  
 TAAAGACTGA CAGTGGCTC CATTGCATA AGAGGACAC TCAGACAAA CTTTGGCTC CTTGTGTGA GACTGACCA  
 960  
 TGTAGAAA TTTCAGACT TCGTACCTC TCTACACTT GAAAACTA TTATCTCAT TATGATTTA ATTCTGCTA  
 1020  
 TGAAGCCAG GATAGTCAA ACAFTTCTC TAAAGGCTA AGTACATGA TAAATATGT AGGCTCTCA GGTCACTTAC  
 1080  
 AGTTTGTCA TGTATCTTT TTCTGCTGC TGTGTGAT ATTGTGTTA CATTGCTTA AAAATATTA AAACCAATC  
 1140  
 ATCACTGAG TCTCAGGCT CCGTGGGAC ACACAGGAC AGCTAAGCT CACTGACAA TACCAAAAT CCACTGACCC  
 1200  
 CCGTCTCTG AAGCTGGCT CCACTGAC CCGTGGGAC ACGAGCTCC AGCGCTCTG GACTTCAAC TCGAGCTCC  
 1260  
 1320  
 1380  
 1440  
 1500  
 1560  
 1600

1680

1760

1840

1920

2000

2080

2160

2240

2320

2000

2480

2560

2660

2720

2800

2890

2960

3040

3126

ZOOLOGICAL CONTRACTS CARRIAGE OF BIOLOGICAL SPECIMENS CONTAINING CREATING AND MANAGING

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1200  
 CCCCCCAGA CTACAGGCT TGGTTAGGG CTGGTTTGT TATTTCAGG ATAAAGCTA GCGACTTCAT CTGGAGGTT  
 1280  
 CTAAGTGGG CAGAGACTAT CAACACACA GGAATCCAG AGGTGGGATC CTCCCTCATG GCTCTGGCAG AGTGTAAATCC  
 1360  
 AAGGGTGGAG ATAGGGAAT GTGAATAGCT GAATCTGTC GGGGAGGCT CCAAGCTCTT CACCTTTCTG GCTCTCTGCT  
 1440  
 CAATGTTGG GTGAGGTAC CTCTCTATC GGGGACAGCC TAGGCTGTTT GGGGTGAAG GGGAGAACTT CTGATTCAG  
 1520  
 CCAATGGAG GAGGGGAGG CAGAGGAGG CCACAGGCA CTCCCTATCT TGTAGTGTT TGGAAATATA CTGTGCAATC  
 1600  
 CCAATAAAA AAAAAGGAG AAAAAATGT AAAAATCAT CTTAGCTTA AGCTACTTAT AGGGGATTA AGCAGGACT  
 1680  
 GTTATGGAG ACAAACTAC ACTTAGAGG AAGAAATAG TTCTGTCCAG CACGCTGTC TCACAGCTCT AACTCCAGCA  
 1760  
 CTITGGGAG CCAAGTGG AGATCTTTT GATTCAGGA GTTGGAGAC AGCTTGACA ACATAGCAAG ATCTTATCTC  
 1840  
 TACAGAAAT TTAATAAAA GAATAAAT AGGCGCAG GTCTOCAGTC CTAGCTACTC GCGAGCTTA GGTGGAGAA  
 1920  
 TCTTGAAGC CAGGATTTA GTTGAAGCT CAGTGAAGT ATGATTGAC CACTGCACTC CAGACTGGT CACTGAATTA  
 2000  
 GACCTGTCT CAAATATAA GAGGACAA GTTCTAGTTT TCAATAGGC AATAAGGTA GTGCTTAG CACAACTA  
 2080  
 TTGTGTAAT CAAATAGCT ACAAGAGAG ATATGAAGT TTGCTCCAA CAGGAAATGA TAACTTGA GGTGACAGT  
 2160  
 ACCTTAATA CCTGATTG ATCAATAC ATCAATGA TGTATCAAA TATTACATGT ACGGACAAA TTGTGTAAA  
 2240  
 TATATCTAT CACTTTTA AGTGGGAG AGCCCAAG CACTCTATC GCTTCCATG GTCACTGTA CCACTGCCAG  
 2320  
 CTCAGCAAT GTATCAGCA AATCTGGG AAGTGGGA ATTGCTTCA TGGCACTAT GCTTTGCA CTATAGGAA  
 2400  
 TGAATTCAG AGATCTTA TCTCAATC GGGACTCTT OCTTCAAGG TTGCTGTC CAGGACATG AGTGACAGT  
 2480  
 AGCTTGGT ACTTACCT GGGGTGAG CAGCAGACA AATGAGCT TGTCTGAG CCAAGCTTC TAGAAACAG  
 2560  
 GCTCTGAG ATCACAAGT ATGCTGGT GAGGCTGA GTTAAATTA GCTGAGGCT TGGGCTTC CAGGCTGTT  
 2640  
 TCTTTGTT CTTCAGTCC AGTCAGATC CATTCTCT GCGAGAGG AGCTTTAGT CACTGTCT GTTCTGAAA  
 2720  
 GCTCTGTA TATTACTGA GTTCTGAG GGGCTGCT TGTCTCTGT CTAAGAAAT AACTACATG TTAAAGAAA  
 2800  
 TATTGAGG GGGGCTAG CTTCAGAC TGTATGAG CACTTGGGA GCGAAGCA GCTGATCAT GAGGTGAG

## Figure 7 cont.

4880  
GTTTCAGACC ATCATGCOCA ACATGCTGAA ACCOCHTTC TACTTAAAT ACATTAATTA CCTGCTGTG CTGCGGZCA

4960  
OCTGVAGTCC CAGCTACTCC CGAGCTGAC CCAGGAAAT COCTTGACC TCGGAGCCG AGGTTCACCT GAGCGATAT

5040  
CAGGCACTG CACTGAGCC TCGGACAGA CCGAGACTCC ATCTCAAAA AAAGAAAAA TAAATACCTG AAATTAAGAC

5120  
TCCCATATA GATTAATAA AATTTATTA AGTAAATAA TAAATATAA AACAGCTCC AGGTCTGATT GCGCCAGAC

5200  
CCTGTAGGAC ACAGACCCG AGCAATGAC TTCATTAAT COGNTOTTA TCAAGCTCAG CTGGAATTT GCGAGCCGA

5280  
CTCATTTTA AACAGTTTC TCGATTCTA CCAACCCAG AAAATCAGAC TCTTTCAGCT AAATTCCTTA CTCTCTCTG

5360  
GATGATGAG GAACAGTTT ATGCTGACC CCAGCTAOC CTCTGAAGA CCGCCACAT CCGCTCTCT CCAGCTCCC

CTCTCTCTC ATTCCCCAG GAGATTTC

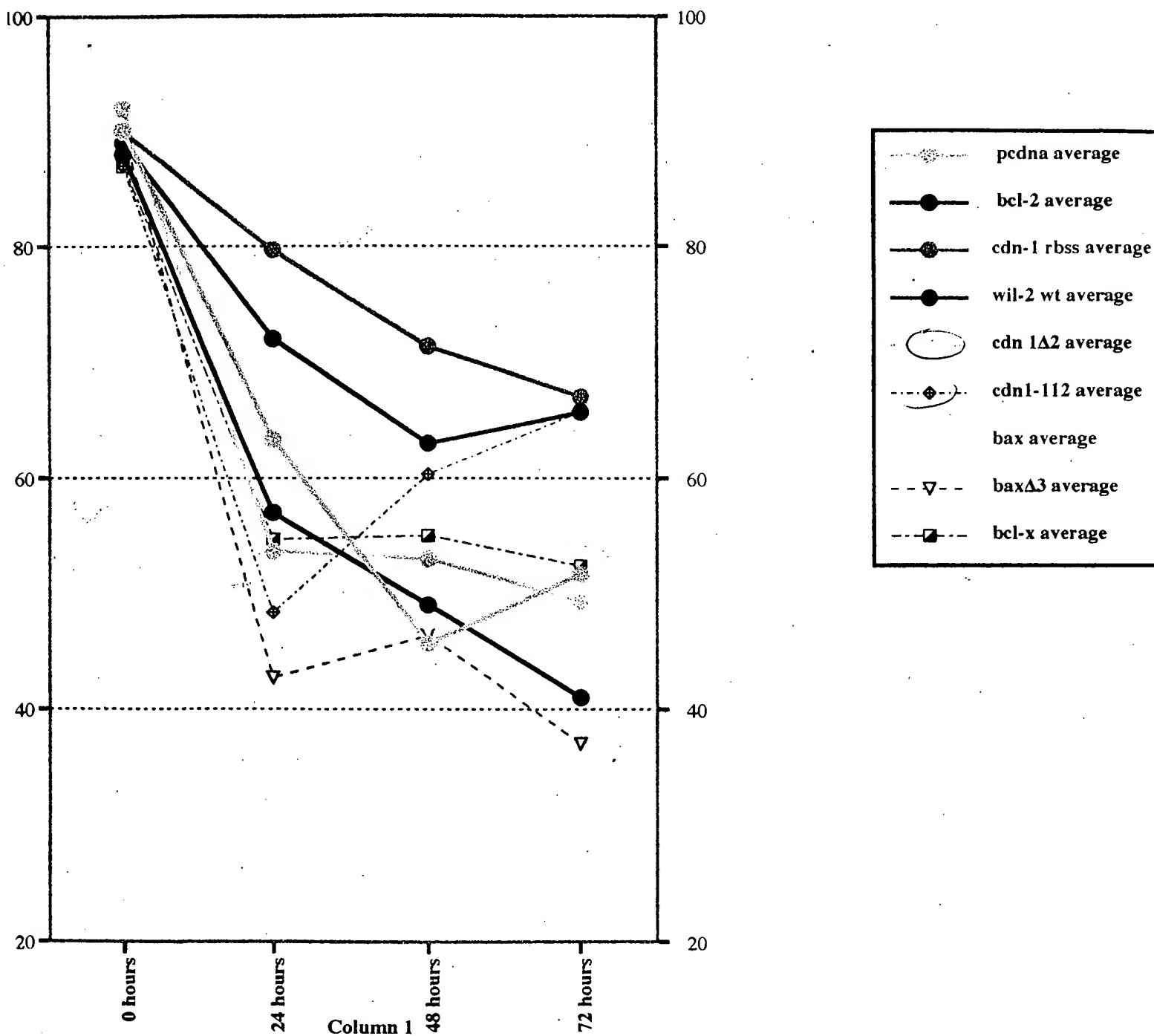




Figure 9

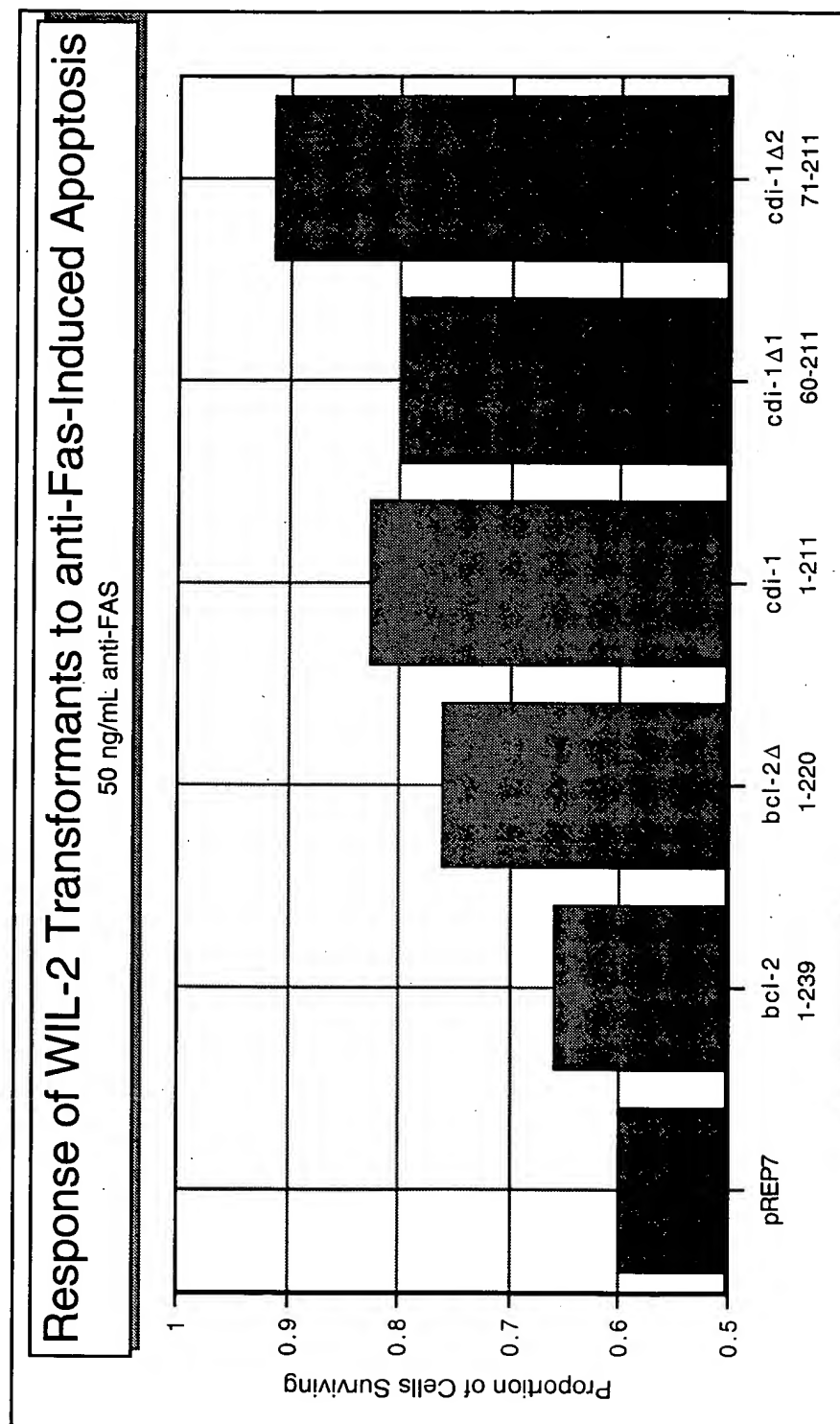


Figure 10

F15.12 transformants - IL-3

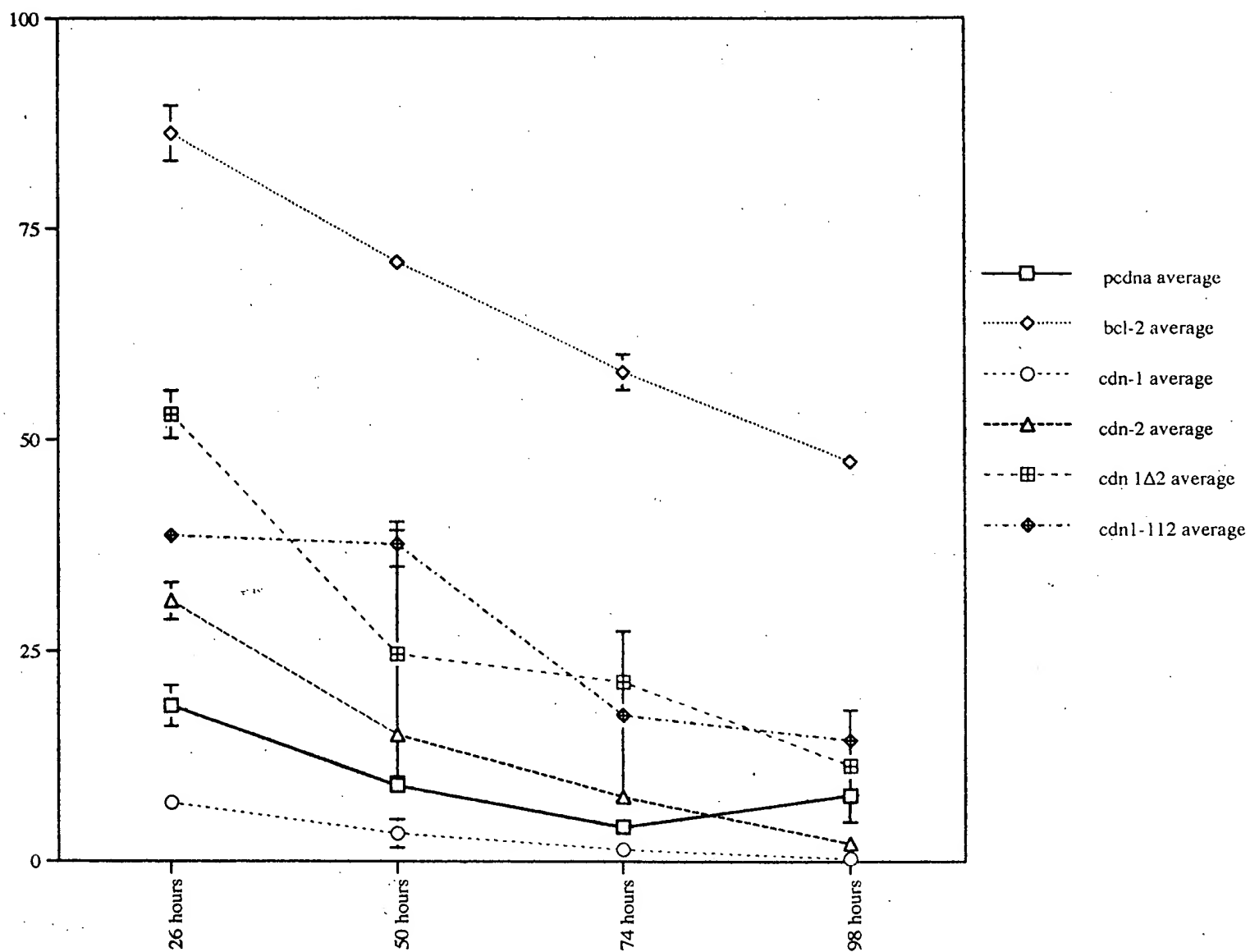


Figure 11 N-terminal methionine residues of cdn-1 derivatives

Δ<sup>2</sup> Δ<sup>3</sup> Δ<sup>1</sup>  
LPLQPSSTMGQVGRQLAIIIGDDINRRYDSEFQTMQLQHLQPTAENAYEYFTKIATSLFESGNWGRVVALLGFGYRLALHVYQHGLTGFLGQVTRFVVDFMLHH  
CIARWIAQORGWVAALNLGNPILNLVVLGVLLGQFVVRFFKS  
MASGQGPGRPRQECGEPALPSASEEQVAQDTEEVFRSYVFYRHQQEQEAEGVAAAPADPEMVT